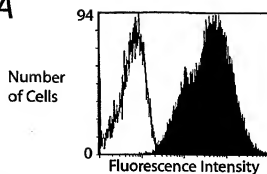


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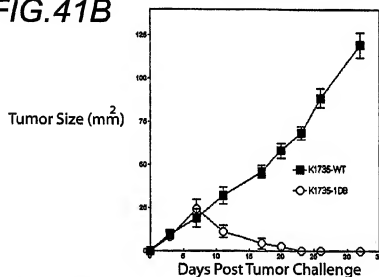
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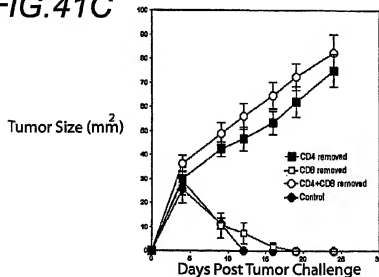
**FIG.41A**



**FIG.41B**



**FIG.41C**

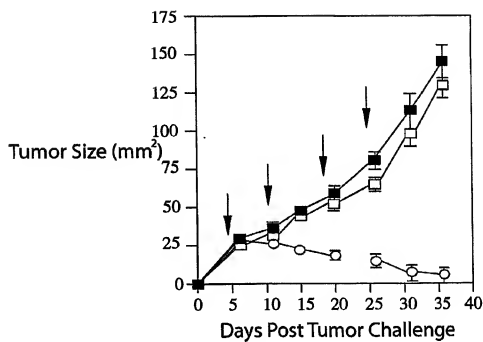


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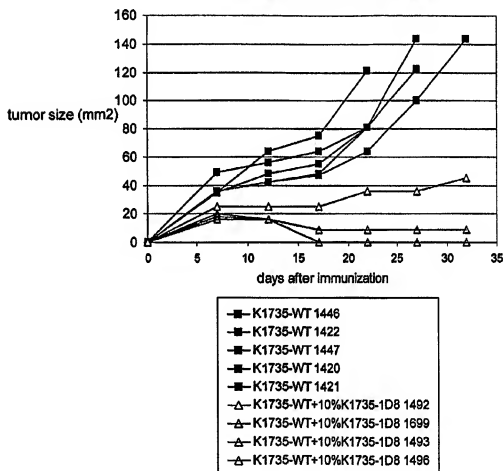
**FIG.42**



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**FIG.43**

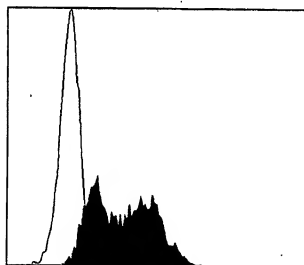
Mixtures of K1735-WT and K1735-1D8 transfected tumor lines  
inhibit tumor outgrowth in C3H mice



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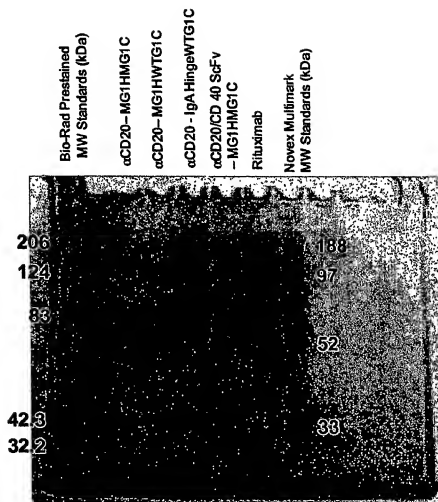
# **FIG.44**

Expression of Anti-CD137 scFvlg on the Surface of  
Panned Ag104 Transfected Tumor Cells



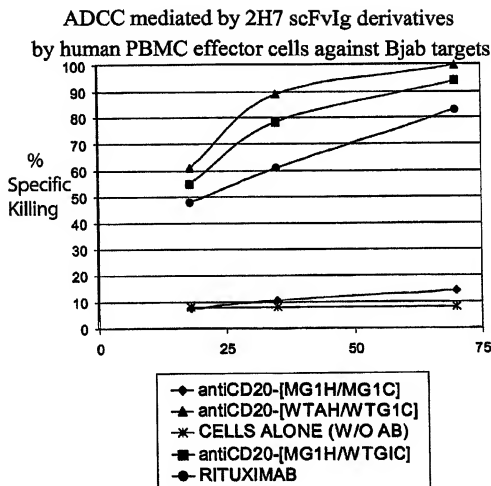
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FIG.45



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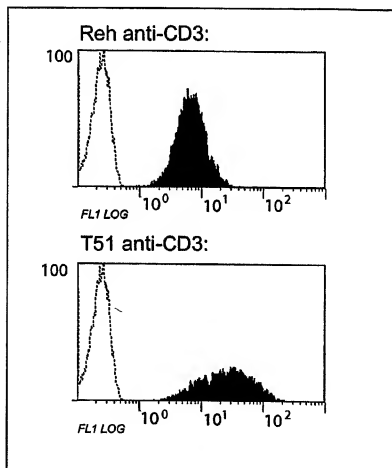
**FIG.46**



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# **FIG.47**

**Cell surface expression of anti-human CD3 scFvIg fusion protein on Reh and T51 Cells.**

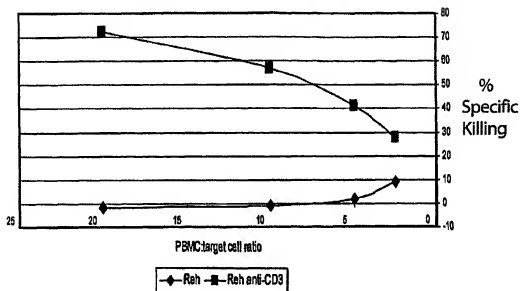


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# FIG. 48A

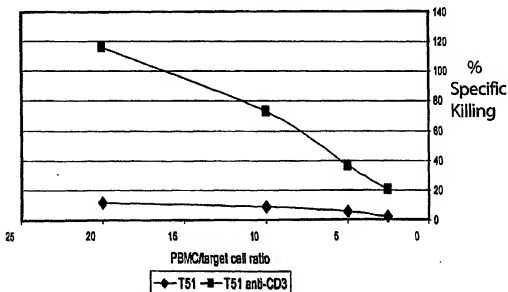
Targeting of Cytotoxicity to Transfected Cell Lines  
by Surface expression of CD3 scFvIg

Cytotoxic activity of resting PBMC towards transfected Reh cells



# FIG. 48B

Cytotoxic activity of resting PBMC towards transfected T51 lymphoblastoid cells



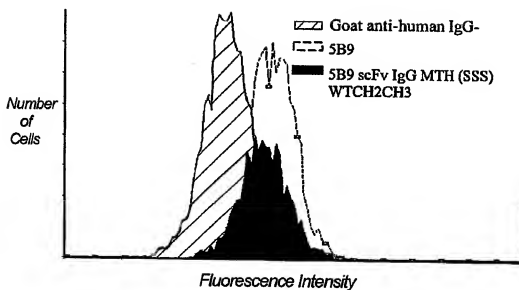


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**FIG. 49**



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      FUNCTION

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480  
ctggtcctaa gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccc  
540  
gagaacaact acaagaccac gccctccgtg ctggactcgc acggctcctt ctctctctac  
600  
agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgtccctgt  
660  
atgcatgagg ctctgcacaa ccactacacg cagaagagcc tctccctgtc tccgggtaaa  
720  
tgatctaga  
729

<210> 8  
<211> 825  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>  
<221> misc\_feature  
<222> (13)..(72)  
<223> LIGHT CHAIN LEADER PEPTIDE



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<220>  
<221> v\_region  
<222> (73)..(405)  
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<220>  
<221> misc\_feature  
<222> (406)..(450)  
<223> SYNTHETIC (GLY4SER)3 LINKER PEPTIDE

<220>  
<221> v\_region  
<222> (454)..(825)  
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD19: HD37

<400> 8  
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ggctccactg gtgacattgt gctgacccaa tctccagctt ctttggctgt gtccttaggg  
120  
cagagggccca ccatctcctg caaggccagc caaagtgttg attatgatgg tgatagttat  
180  
ttgaactggt accaacagat tccaggacag ccacccaac tcctcatcta tgatgatcc  
240  
aatctagtgt ctgggatccc acccagggtt agtggcagtg ggtctgggac agacttcacc  
300  
ctcaacatcc atcctgtgga gaaggtggat gctgcaacct atcactgtca gcaaagtact  
360  
gaggatccgt ggacgttcgg tggaggcacc aagctggaaa tcaaaggctg cgggtgctcg  
420  
ggcggtggtg ggtcgggtgg cgcgggatcg tcacagggtc agctgcagca gtcctgggct  
480  
gagctggtag ggcctgggtc ctcagtgaag atttctcgca aggcttctgg ctatgcattc  
540  
agtagctact ggatgaactg ggtgaagcag aggcctggac agggctcttga gtggattgga  
600  
cagatttggt ctggagatgg tgatactaac tacaatggaa agttcaaggg taaagccact  
660  
ctgactgcag acgaatcttc cagcacagcc tacatgcaac tcagcagcct agcatctgag  
720  
gactctgcgg tctatttctg tgcaagacgg gagactacga cggtaggccc ttattactat  
780  
gctatggact actgggggtca aggaacctca gtcaccgtct ctcca  
825

<210> 9  
<211> 795  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> SYNTHETIC MOUSE SCFV FUSION GENE

<220>  
<221> misc\_feature  
<222> (13)..(72)  
<223> LIGHT CHAIN LEADER PEPTIDE SEQUENCE

<220>  
<221> v\_region  
<222> (73)..(393)  
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<220>  
<221> misc\_feature  
<222> (394)..(441)  
<223> SYNTHETIC LINKER PEPTIDE ENCODED (GLY4SER)3

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<220>
<221> V_region
<222> (442)..(795)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD37: G28-1

<400> 9
aagcttgccg ccatgggtatc cacagctcag ttccttgggt tgctgctgct gtggcttaca
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ggtaggcagat gtgacatcca gatgactcag tctccagcct ccttatctgc atctgtggga
120
ggagactgtca ccatcacatg tcgaacaagt gaaatgttt acagttattt ggcttggtat
180
cagcagaaaac agggaaaatc tctcagctc ctggctcttt ttgcaaaaac cttagcagaa
240
gggtgtccat caaggttcag tggcagtga tcaggcacac agttttctct gaagatcagc
300
agcctgcagc ctgaagattc tggaggttat ttctgtcaac atcattccga taatccgtgg
360
acgttcggtg gaggcaccga actggagatc aaaggtggcg gtggctcggg cgggtggtggg
420
tcgggtggcg gcggatcgtc agcgggtccag ctgcagcagt ctggacctga gctggaaaag
480
cctggcgctt cagtgaagat ttctgcaag gcttctggtt actcattcac tggctacaat
540
atgaactggg tgaagcagaa taatggaag agccttgagt ggattggaaa tattgatcct
600
tattatgggt gtactaccta caaccggaag ttcaagggca aggccacatt gactgtagac
660
aaattcctca gcacagccta catgcagctc aagagtctga catctgagga ctctgcagtc
720
tattactgtg caagatcggg cgccctatg gactactggg gtcaaggaac ctcatgacc
780
gtctcttctg atcag
795

<210> 10
<211> 824
<212> DNA
<213> Artificial Sequence

<220>
<223> SYNTHETIC MOUSE FUSION GENE

<220>
<221> sig_peptide
<222> (1)..(61)
<223> native light chain leader peptide

<220>
<221> V_region
<222> (62)..(397)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>
<221> misc_feature
<222> (398)..(445)
<223> (gly4ser)3 linker peptide

<220>
<221> V_region
<222> (445)..(818)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD22: G28-7

<220>
<221> misc_feature
<222> (819)..(824)
<223> BclI restriction site

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<400> 10
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60
aacattatga tgacacagtc gccatcatct ctggctgtgt cagcaggaga aaaggtcact
120
atgaactgta agtccagtc aagtgttttc tacagttaa atcagaggaa ttatttggcc
180
tggtatcagc agaaaccagg gcagtcctcc aaattgctga tctactgggc atctactagg
240
gaatctgggtg tccctgatcg cttcacaggc agtggatccg ggacagactt tactcttacc
300
atcagcagtg tacatactga agacctggca gtttattact gtcataaatt cctctcttcg
360
tggacgttcg gtggaggcac caagctggaa atcaaaaggcg gtggtgggtc ggggtgggtg
420
gggtcgggtg gcggcggtc ttctcaggtc caactgcagc agcctggggc tgaactgggtg
480
aagcctggga cttcagtgaa gctgtcctgc aaggcctctg gctacacctt caccaactac
540
tggatggctt ggggtgaagca gacgcctgga gaagcccttg agtggattgg agaaaattatt
600
cctagcaacg gtcgtactaa atacaatgag aagttaaga gcaaggccac actgactgca
660
gacaaatcct cccgcacagc ctacatgcaa ctcagcagcc tggcatctga ggactctgcg
720
gtctattatt gtgaagaga gatgtccatt attactacgg tactgactcc cggtttgctt
780
actggggcca agggactctg gtcactgtct ctgcagcctg atca
824
```

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<210> 11
<211> 266
<212> PRT
<213> Mus musculus
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<220>
<221> INIT_MET
<222> (1)..(1)
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<220>
<221> SIGNAL
<222> (1)..(2)
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<220>
<221> DOMAIN
<222> (23)..(128)
<223> LIGHT CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20
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```
<220>
<221> SITE
<222> (129)..(144)
<223> ASP-(GLY3SER)-(GLY4SER)2-SER LINKER PEPTIDE
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<220>
<221> DOMAIN
<222> (145)..(266)
<223> HEAVY CHAIN VARIABLE DOMAIN FOR MOUSE ANTI-HUMAN CD20
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<400> 11
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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
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50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Thr Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
225 230 235 240  
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Val Thr Val Ser Asp  
260 265

<210> 12  
<211> 271  
<212> PRT  
<213> Mus musculus

<220>  
<221> SITE  
<222> (1)..(271)  
<223> MOUSE ANTI-HUMAN CD19 SCFV

<400> 12

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
1 5 10 15  
Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala  
20 25 30  
Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser  
35 40 45  
Val Asp Tyr Asp Gly Asp Ser Tyr Leu Asn Trp Tyr Gln Gln Ile Pro  
50 55 60  
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Val Ser  
65 70 75 80  
Gly Ile Pro Pro Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
85 90 95  
Leu Asn Ile His Pro Val Glu Lys Val Asp Ala Ala Thr Tyr His Cys  
100 105 110  
Gln Gln Ser Thr Glu Asp Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu  
115 120 125  
Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
130 135 140  
Gly Ser Ser Gln Val Gln Leu Gln Ser Gly Ala Glu Leu Val Arg  
145 150 155 160  
Pro Gly Ser Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe  
165 170 175  
Ser Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
180 185 190  
Glu Trp Ile Gly Gln Ile Trp Pro Gly Asp Gly Asp Thr Asn Tyr Asn  
195 200 205  
Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Glu Ser Ser Ser  
210 215 220  
Thr Ala Tyr Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
225 230 235 240  
Tyr Phe Cys Ala Arg Arg Glu Thr Thr Thr Val Gly Arg Tyr Tyr Tyr  
245 250 255  
Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser  
260 265 270

<210> 13  
<211> 259  
<212> PRT  
<213> Mus musculus

<220>  
<221> SITE  
<222> (1)..(259)  
<223> MOUSE ANTI-HUMAN CD37 SCFV

<400> 13

Met Val Ser Thr Ala Gln Phe Leu Gly Leu Leu Leu Leu Trp Leu Thr  
1 5 10 15  
Gly Gly Arg Cys Asp Ile Gln Met Thr Thr Ser Pro Ala Ser Leu Ser  
20 25 30  
Ala Ser Val Gly Glu Thr Val Thr Thr Cys Arg Thr Ser Glu Asn  
35 40 45  
Val Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro  
50 55 60  
Gln Leu Leu Val Ser Phe Ala Lys Thr Leu Ala Glu Gly Val Pro Ser  
65 70 75 80  
Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Ser  
85 90 95  
Ser Leu Gln Pro Glu Asp Ser Gly Ser Tyr Phe Cys Gln His His Ser  
100 105 110  
Asp Asn Pro Trp Thr Phe Gly Gly Gly Thr Glu Leu Glu Ile Lys Gly  
115 120 125  
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser Ala  
130 135 140  
Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Glu Lys Pro Gly Ala Ser  
145 150 155 160  
Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Asn  
165 170 175  
Met Asn Trp Val Lys Gln Asn Asn Gly Lys Ser Leu Glu Trp Ile Gly  
180 185 190  
Asn Ile Asp Pro Tyr Tyr Gly Gly Thr Thr Tyr Asn Arg Lys Phe Lys  
195 200 205  
Gly Lys Ala Thr Leu Thr Val Asp Gly Ser Ser Ser Thr Ala Tyr Met  
210 215 220  
Gln Leu Lys Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala  
225 230 235 240  
Arg Ser Val Gly Pro Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr  
245 250 255  
Val Ser Ser

<210> 14  
<211> 272  
<212> PRT  
<213> Mus musculus

<220>  
<221> SITE  
<222> (1)..(272)  
<223> MOUSE ANTI-HUMAN CD22 SCFV

<400> 14

Met Glu Ser His Ser Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser  
1 5 10 15  
Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala

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Val	20	Ser	35	Ala	40	Gly	45	Glu	50	Lys	55	Val	60	Thr	65	Met	70	Asn	75	Cys	80	Lys	85	Ser	90	Gln	95	Ser	100
Val	105	Phe	110	Tyr	115	Ser	120	Ser	125	Asn	130	Gln	135	Arg	140	Asn	145	Tyr	150	Leu	155	Ala	160	Trp	165	Tyr	170	Gln	175
Lys	180	Pro	185	Gly	190	Gln	195	Ser	200	Pro	205	Lys	210	Leu	215	Leu	220	Ile	225	Tyr	230	Trp	235	Ala	Ser	240	Thr	245	Arg
Glu	250	Ser	255	Gly	260	Val	265	Pro	270	Asp	275	Arg	Phe	280	Thr	285	Gly	290	Ser	295	Gly	Ser	Gly	Ser	Gly	300	Thr	305	Asp
Phe	310	Thr	315	Leu	320	Thr	325	Ile	330	Ser	335	Ser	340	Val	345	His	350	Thr	355	Glu	360	Asp	365	Leu	370	Ala	375	Val	380
Tyr	385	Cys	390	His	395	Gln	400	Phe	405	Leu	410	Ser	415	Ser	420	Trp	425	Thr	430	Phe	435	Gly	440	Gly	445	Thr	450	Lys	455
Leu	460	Glu	465	Ile	470	Lys	475	Gly	480	Gly	485	Gly	490	Ser	495	Gly	500	Gly	505	Gly	510	Pro	515	Gly	520	Ala	525	Glu	530
Gly	535	Thr	540	Ser	545	Ser	550	Gln	555	Val	560	Gln	565	Leu	570	Gln	575	Gln	580	Pro	585	Gly	590	Ala	595	Glu	600	Val	605
Lys	610	Pro	615	Gly	620	Thr	625	Ser	630	Val	635	Lys	640	Leu	645	Ser	650	Cys	655	Lys	660	Ala	665	Ser	670	Gly	675	Tyr	680
Phe	685	Thr	690	Asn	695	Tyr	700	Trp	705	Met	710	Val	715	Trp	720	Val	725	Lys	730	Gln	735	Thr	740	Pro	745	Gly	750	Thr	755
Leu	760	Glu	765	Trp	770	Ile	775	Gly	780	Glu	785	Ile	790	Ile	795	Pro	800	Ser	805	Asn	810	Gly	815	Arg	820	Lys	825	Tyr	830
Asn	835	Glu	840	Lys	845	Phe	850	Lys	855	Ser	860	Lys	865	Ala	870	Thr	875	Leu	880	Thr	885	Ala	890	Asp	895	Lys	900	Ser	905
Arg	910	Thr	915	Ala	920	Tyr	925	Met	930	Gln	935	Leu	940	Ser	945	Ser	950	Leu	955	Ala	960	Ser	Glu	965	Asp	970	Ser	975	Ala
Val	980	Tyr	985	Tyr	990	Cys	995	Ala	1000	Arg	1005	Glu	1010	Met	1015	Ser	1020	Ile	1025	Thr	1030	Thr	1035	Val	1040	Leu	1045	Thr	1050
Pro	1055	Gly	1060	Leu	1065	Leu	1070	Thr	1075	Gly	1080	Ala	1085	Lys	1090	Gly	1095	Leu	1100	Trp	1105	Ser	1110	Leu	1115	Ser	1120	Leu	1125

<210> 15  
 <211> 499  
 <212> PRT  
 <213> Artificial Sequence  
 <220>  
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN  
 <220>  
 <221> SITE  
 <222> (1)..(265)  
 <223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7  
 <220>  
 <221> DOMAIN  
 <222> (266)..(499)  
 <223> HUMAN IGG1 WILD TYPE HINGE, CH2, CH3 FC

<400> 15

Met	1	Asp	5	Phe	10	Gln	15	Val	20	Gln	25	Ile	30	Phe	35	Ser	40	Leu	45	Leu	50	Ile	55	Ser	60	Ala	65	Ser	70
Val	75	Ile	80	Ile	85	Ala	90	Arg	95	Gly	100	Gln	105	Ile	110	Val	115	Leu	120	Ser	125	Gln	130	Ser	135	Pro	140	Ala	145
Leu	150	Ser	155	Ala	160	Ser	165	Pro	170	Gly	175	Glu	180	Lys	185	Val	190	Thr	195	Met	200	Thr	205	Cys	210	Arg	215	Ala	220
Ser	225	Ser	230	Val	235	Ser	240	Tyr	245	Met	250	His	255	Trp	260	Tyr	265	Gln	270	Gln	275	Lys	280	Pro	285	Gly	290	Ser	295
Pro	300	Lys	305	Pro	310	Trp	315	Ile	320	Tyr	325	Ala	330	Pro	335	Ser	340	Asn	345	Leu	350	Ala	355	Ser	360	Gly	365	Val	370
Ala	375	Arg	380	Phe	385	Ser	390	Gly	395	Ser	400	Gly	405	Ser	410	Thr	415	Ser	420	Tyr	425	Ser	430	Leu	435	Thr	440	Ile	445
Ser	450	Arg	455	Val	460	Glu	465	Ala	470	Glu	475	Asp	480	Ala	485	Ala	490	Thr	495	Tyr	500	Tyr	Cys	505	Gln	510	Gln	515	Trp
Ser	520	Phe	525	Asn	530	Pro	535	Pro	540	Thr	545	Phe	550	Ala	555	Gly	560	Thr	565	Lys	570	Leu	575	Glu	580	Leu	585	Lys	590

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 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
 180 185 190  
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
 210 215 220  
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
 225 230 235 240  
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Cys  
 260 265 270  
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 275 280 285  
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 290 295 300  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 305 310 315 320  
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 325 330 335  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 340 345 350  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 355 360 365  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 370 375 380  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 385 390 395 400  
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 405 410 415  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 420 425 430  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Pro Pro  
 435 440 445  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 450 455 460  
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 465 470 475 480  
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 485 490 495  
 Pro Gly Lys

<210> 16  
 <211> 499  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>  
 <221> SITE  
 <222> (1)..(265)  
 <223> 2H7 SCFV TARGETED TO HUMAN CD20

<220>  
 <221> DOMAIN  
 <222> (265)..(499)  
 <223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)  
 PROLINE IN CH2 MUTATED TO SERINE (AMINO ACID 290)

<400> 16

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 10 15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20 25 30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35 40 45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50 55 60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80
Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85 90 95
Ser Arg Val Glu Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100 105 110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115 120 125
Asp Gly Gly Gly Ser Gly Gly Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
130 135 140 145
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
150 155 160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165 170 175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180 185 190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195 200 205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210 215 220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225 230 235 240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245 250 255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
260 265 270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275 280 285
Gly Ser Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290 295 300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
305 310 315 320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325 330 335
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
340 345 350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355 360 365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370 375 380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385 390 395 400
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
405 410 415 420
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
425 430 435
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
440 445 450
Val Leu Asp Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val
455 460 465
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
470 475 480 485
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
490 495
Pro Gly Lys

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<210> 17  
<211> 499  
<212> PRT



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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<213> Artificial Sequence

<220>

<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>

<221> SITE

<222> (1)..(265)

<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>

<221> DOMAIN

<222> (266)..(499)

<223> HINGE CYSTEINES MUTATED TO SERINES (AMINO ACIDS 272, 278, 281)  
CH2 AND CH3 DOMAINS ARE WILD TYPE IN SEQUENCE

<400> 17

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1      5      10      15
Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
20      25      30
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100      105      110
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115      120      125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245      250      255
Gly Thr Gly Thr Val Thr Val Ser Asp Gln Glu Pro Lys Ser Ser
260      265      270
Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly
275      280      285
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
290      295      300
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His
305      310      315      320
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
325      330      335
His Asn Ala Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
340      345      350
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
355      360      365
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
370      375      380
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
385      390      395      400

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
405 410 415  
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
420 425 430  
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
435 440 445  
Val Leu Asp Ser Asp Gly Ser Phe Leu Tyr Ser Lys Leu Thr Val  
450 455 460  
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
465 470 475 480  
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
485 490 495  
Pro Gly Lys

<210> 18  
<211> 505  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> MOUSE-HUMAN FUSION PROTEIN

<220>  
<221> SITE  
<222> (1)..(265)  
<223> MOUSE ANTI-HUMAN CD20 SCFV: 2H7

<220>  
<221> DOMAIN  
<222> (266)..(288)  
<223> WILD TYPE IGA HINGE

<220>  
<221> DOMAIN  
<222> (289)..(505)  
<223> HUMAN IGG1 CH2 AND CH3 DOMAINS, WILD TYPE SEQUENCE

<400> 18  
Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
1 5 10 15  
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20 25 30  
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
35 40 45  
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser  
50 55 60  
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro  
65 70 75 80  
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
85 90 95  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
100 105 110  
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
115 120 125  
Asp Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser  
130 135 140  
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala  
145 150 155 160  
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
165 170 175  
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
180 185 190  
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
195 200 205  
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
210 215 220  
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
225 230 235  
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
245 250 255  
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Gln Pro Val Pro Ser Thr  
260 265 270  
Pro Pro Thr Pro Ser Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Cys  
275 280 285  
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys  
290 295 300  
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
305 310 315 320  
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr  
325 330 335  
Val Asp Gln Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu  
340 345 350  
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His  
355 360 365  
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
370 375 380  
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln  
385 390 395 400  
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu  
405 410 415  
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro  
420 425 430  
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
435 440 445  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu  
450 455 460  
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
465 470 475 480  
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
485 490 495  
Lys Ser Leu Ser Leu Ser Pro Gly Lys  
500 505

<210> 19

<211> 234

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (1)..(234)

<223> MUTANT IGG1 HINGE (AMINO ACIDS 7, 13, 16)

WILD TYPE CH2 AND CH3 DOMAINS

ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<400> 19

Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser  
1 5 10 15  
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
20 25 30  
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
35 40 45  
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
50 55 60  
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
65 70 75 80  
Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
85 90 95  
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
100 105 110  
Lys Ala Leu Pro Ala Pro Ile Glu Thr Ile Ser Lys Ala Lys Gly  
115 120 125  
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu  
130 135 140  
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
145 150 155 160  
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
165 170 175  
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
180 185 190  
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
195 200 205  
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
210 215 220  
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<210> 20  
<211> 240  
<212> PRT  
<213> Homo sapiens

<220>  
<221> SITE  
<222> (1)..(23)  
<223> ALTERNATIVE CARBOXY TERMINUS OF SCFVIG FUSION PROTEINS

<220>  
<221> DOMAIN  
<222> (24)..(240)  
<223> HUMAN IGG1 WILD TYPE CH2 AND CH3 FC

<400> 20

Asp Gln Pro Val Pro Ser Thr Pro Pro Thr Pro Ser Pro Ser Thr Pro  
1 5 10 15  
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20 25 30  
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg  
35 40 45  
Thr Pro Glu Val Thr Cys Val Val Asp Val Ser His Glu Asp Pro  
50 55 60  
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala  
65 70 75 80  
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val  
85 90 95  
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr  
100 105 110  
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr  
115 120 125  
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
130 135 140  
Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys  
145 150 155 160  
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
165 170 175  
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
180 185 190  
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
195 200 205  
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
210 215 220  
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
225 230 235 240

<210> 21  
<211> 1470  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> MOUSE-HUMAN HYBRID

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

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<220>
<221> misc_feature
<222> (1)..(808)
<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>
<221> misc_feature
<222> (814)..(1455)
<223> HUMAN EXTRACELLULAR DOMAIN LONG FORM, CD154

<400> 21
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60
gtcataattg ccaggaggaca aattgtttctc tcccagcttc cagcaatcct gttcgtcatct
120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgactagg
180
taccagcaga agccaggatc ctcccccaaa ccttggaatt atgccccatc caactggct
240
tctggagctc ctgctcgctt cagtggcagt ggtctggga cctcttactc tctcaaatc
300
agcagagtgg aggctgaaga tgctgccact tattactgcc agcagtggag ttttaacca
360
cccacgttcg gtgctgggac caagctggag ctgaagaatg cggttggttc gggcggtggt
420
ggactctggag gagtggggag ctctcaggct tatctacagc agtctggggc tgagctggtg
480
agggctgggg cctcagtgaa gatgtcctgc aaggcttctg gctacacatt taccagttac
540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat
600
caggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta
660
gacaaatcct ccagcacagc ctacatcgag ctacagagcc tgacatctga agactctgcg
720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cagtgtctgg
780
ggcagcaggga ccacggtcac cgtctctgat ccaagaaggt tggacaagat agaagatgaa
840
aggaaatctc atgaagattt tgtattcatg aaaacgatac agagatgcaa cacaggagaa
900
agatccttat ctttactgaa ctgtgaggag attaaaagcc agtttgaagg ctttggtaag
960
gatataatgt taaacaaaga ggagacgaag aaagaaaaca gctttgaaat gcaaaaaggt
1020
gatcagatc ctcaaatgac ggcacatgac ataagtgagg ccagcagtaa aacaacatct
1080
gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggt aacctggaa
1140
aatgggaaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtacc
1200
ttctgttcca atcggaagac ttcgagtcaa gctccattta tagccagcct ctgcctaaag
1260
tccccgggta gattcgagag aatcttactc agagctgcaa ataccacagc ttccgccaaa
1320
ccttgcgggc aacaatccat tcacttggga ggagttattg aattgcaacc aggtgcttgc
1380
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cagctccttt
1440
ggcttactca aactcgagtg ataacttaga
1470

<210> 22
<211> 1290
<212> DNA
<213> Artificial Sequence

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>  
<223> MOUSE-HUMAN HYBRID

<220>  
<221> misc\_feature  
<222> (13)..(808)  
<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>  
<221> misc\_feature  
<222> (814)..(1275)  
<223> HUMAN EXTRACELLULAR DOMAIN, SHORT FORM, CD154

<400> 22  
aagcttgccg ccattgattt tcaagtgcag attttcagct tctgctaatt cagtgttca  
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gtcataattg ccaggaggaca aattgttctc tccagctctc cagcaatcct gtctgcatct  
120  
ccaggggaga aggtcacaat gacttgagg gccagctcaa gtgtaagtta catgactagg  
180  
taccagcaga agccaggatc ctcccccaaa ccttgagatt atgccccatc caactgggt  
240  
tctggagctc ctgctcgctt cagtggcagt ggtctggga cctcttactc tctcacaatc  
300  
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaacca  
360  
cccagcttg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggt  
420  
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt  
480  
aggctgggg cctcagtgaa gatgtcctgc aagccttctg gctacacatt taccagttac  
540  
aatatgcact gggtaaaaga gacacctaga cagggccttg aatggattgg agctatttat  
600  
ccaggaaaatg gtgatacttc ctacaatcag aagtccaagg gcaaggccac actgactgta  
660  
gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgag  
720  
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgaagtctgg  
780  
ggcacaggga ccacgggtcac cgtctctgat ccagaaaaca gctttgaaat gcaaaaagggt  
840  
gatcagaatc ctcaaattgc ggcacatgtc ataagtgagg ccagcagtaa aacaacatct  
900  
gtgttacagt gggctgaaaa aggatactac accatgagca acaacttggt aacctggaa  
960  
aatgggaac agctgaccgt taaaagacaa ggactctatt atatctatgc ccaagtcaac  
1020  
ttctgttcca atcggaagc ttcgagtcga gctccattta tagccagcct ctgcctaaag  
1080  
tccccgggta gattcgagag aatcttactc agagctgcaa ataccacag ttccgccaaa  
1140  
ccttgcgggc aacaatccat tcaactggga ggagattttg aattgcaacc aggtgcttcg  
1200  
gtgtttgtca atgtgactga tccaagccaa gtgagccatg gcactggctt cagctccttt  
1260  
ggcttactca aactcgagtg ataactcaga  
1290

<210> 23  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 23

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
gtcaagcttg ccgccatgga ttttcaagtg cagatttttc agc  
43

<210> 24  
<211> 74  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 24  
gtcgtcgagc tcccacctcc tccagatcca ccaccgccc agccaccgcc accttcagc  
60  
tccagcttg tccc  
74

<210> 25  
<211> 37  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 25  
gctgctgagc tctcaggctt atctacagca agtctgg  
37

<210> 26  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 26  
gttgctgat cagagacggt gaccgtggtc cc  
32

<210> 27  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE

<400> 27  
gttgctggat ccagaaaaca gctttgaaat gcaa  
34

<210> 28  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
<223> OLIGONUCLEOTIDE

<400> 28  
gttgtttcta gattatcact cgagtttgag taagccaaag gacg  
44

<210> 29  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE  
  
<400> 29  
gttgtcggat ccaagaaggt tggacaagat agaag  
35

<210> 30  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE  
  
<400> 30  
gtctatataa gcagagctct ggc  
23

<210> 31  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE  
  
<400> 31  
cgaggctgat cagcgagctc tagca  
25

<210> 32  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> OLIGONUCLEOTIDE  
  
<400> 32  
ccgcaatttg aggattctga tcacc  
25

<210> 33  
<211> 482  
<212> PRT  
<213> Artificial Sequence



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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<220>  
<223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>  
<221> SITE  
<222> (1)..(266)  
<223> MOUSE ANTI-HUMAN CD20 SCFV

<220>  
<221> DOMAIN  
<222> (268)..(481)  
<223> EXTRACELLULAR DOMAIN, LONG FORM, HUMAN CD154

<400> 33

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Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1      5      10      15
Val Ile Ile Ala Arg Gly Gln Ile Val Ser Gln Ser Pro Ala Ile
20
Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
35      40      45
Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
50      55      60
Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
65      70      75      80
Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
85      90      95
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
100
Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
115      120      125
Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
130      135      140
Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
145      150      155      160
Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
165      170      175
Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
180      185      190
Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
195      200      205
Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
210      215      220
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
225      230      235      240
Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
245      250      255
Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Arg Arg Leu Asp Lys
260      265      270
Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr
275      280      285
Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn Cys
290      295      300
Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu
305      310      315
Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys Gly
320      325      330
Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser
335      340      345
Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Thr Met
350      355      360
Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys
365      370      375
Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn
380      385      390      395
Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala ser Leu Cys Leu Lys
400      405      410      415
Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His
420      425      430

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49076.000004pct2 10.207.655 seq List Text 07.24.03.txt  
 Ser Ser Ala Lys Pro Cys Gly Gln Ser Ile His Leu Gly Gly Val  
 435 440 445  
 Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro  
 450 455 460  
 Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys  
 465 470 475 480  
 Leu Glu

<210> 34  
 <211> 422  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> MOUSE-HUMAN HYBRID FUSION PROTEIN

<220>  
 <221> SITE  
 <222> (1)..(266)  
 <223> MOUSE ANTI-HUMAN SCFV

<220>  
 <221> DOMAIN  
 <222> (268)..(421)  
 <223> EXTRACELLULAR DOMAIN, SHORT FORM, HUMAN CD154

<400> 34

Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser  
 1 10 15  
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile  
 20 25 30  
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser  
 35 40 45  
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 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Lys  
 115 120 125  
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser  
 130 135 140  
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 145 150 155 160  
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
 165 170 175  
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile  
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 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe  
 195 200 205  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr  
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 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp  
 245 250 255  
 Gly Thr Gly Thr Thr Val Thr Val Ser Asp Pro Glu Asn Ser Phe Glu  
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340 345 350  
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala  
355 360 365  
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His  
370 375 380  
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn  
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<213> Homo sapiens  
  
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<221> N\_region  
<222> (1)..(63)  
<223> PORTION OF HUMAN IGA HINGE DOMAIN CONTAINING ONLY 1 CYSTEINE

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tgc  
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<212> PRT  
<213> Homo sapiens  
  
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Pro Ser Pro Ser Cys  
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<210> 37  
<211> 763  
<212> DNA  
<213> Homo sapiens  
  
<220>  
<221> misc\_feature  
<222> (1)..(6)  
<223> BCLI SITE FOR FUSION TO AMIN TERMINAL SCFVS

<220>  
<221> N\_region  
<222> (8)..(752)  
<223> WILD TYPE IGA HINGE, CH2, CH3 DOMAINS  
TRUNCATED TO REMOVE SECRETORY COMPONENT ATTACHMENT

<400> 37  
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 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> DOMAIN  
 <222> (3)..(250)  
 <223> TRUNCATED FORM, REMOVAL OF LAST THREE AMINO ACIDS THAT MEDIATE  
 ATTACHMENT TO SECRETORY COMPONENT

<400> 38

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Pro	Ala	Leu	Glu	Asp	Leu	Leu	Leu	Gly	Ser	Glu	Ala	Ile	Leu	Thr	Cys
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Thr	Leu	Thr	Gly	Leu	Arg	Asp	Ala	Ser	Gly	Val	Thr	Phe	Thr	Trp	Thr
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Pro	Ser	Ser	Gly	Lys	Ser	Ala	Val	Gln	Gly	Pro	Pro	Asp	Arg	Asp	Leu
				70					75					80	
Cys	Gly	Cys	Tyr	Ser	Val	Ser	Ser	Val	Leu	Pro	Gly	Cys	Ala	Glu	Pro
			85						90					95	
Trp	Asn	His	Gly	Lys	Thr	Phe	Thr	Cys	Thr	Ala	Ala	Tyr	Pro	Glu	Ser
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Lys	Thr	Pro	Leu	Thr	Ala	Thr	Leu	Ser	Lys	Ser	Gly	Asn	Thr	Phe	Arg
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Pro	Glu	Val	His	Leu	Leu	Pro	Pro	Pro	Ser	Glu	Glu	Leu	Ala	Leu	Asn
			130				135				140				
Glu	Leu	Val	Thr	Leu	Thr	Cys	Leu	Ala	Arg	Gly	Phe	Ser	Pro	Lys	Asp
			145				150			155				160	
Val	Leu	Val	Arg	Trp	Leu	Gln	Gly	Ser	Gln	Glu	Leu	Pro	Arg	Glu	Lys
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Tyr	Leu	Thr	Trp	Ala	Ser	Arg	Gln	Glu	Pro	Ser	Gln	Gly	Thr	Thr	Thr
			180				185						190		
Phe	Ala	Val	Thr	Ser	Ile	Leu	Arg	Val	Ala	Ala	Glu	Asp	Trp	Lys	Lys
			195				200					205			
Gly	Asp	Thr	Phe	Ser	Cys	Met	Val	Gly	His	Glu	Ala	Leu	Pro	Leu	Ala
			210			215					220				
Phe	Thr	Gln	Lys	Thr	Ile	Asp	Arg	Leu	Ala	Gly	Lys	Pro	Thr	His	Val
			225			230				235				240	
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<400> 39  
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<210> 40  
<211> 4  
<212> PRT  
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<223> Sequence contained in the core hinge region of human IgG1.

<400> 40  
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<210> 41  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Human IgA-derived hinge.

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Pro Thr Ser Pro Val Pro Gln Asp  
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<210> 42  
<211> 1593  
<212> DNA  
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ccggcgagc cgggctctgg aggaagaaag agtttgcga ggcagcagta acaagctcac 360  
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gtgtgtctct ggaatttgg aattaccta tgtgcagag aattatgatc ttctctct 480  
aaagaccatc caggaggtgg ctggttatgt cctcattgcc ctcaacacag tggagcgaat 540  
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 <212> PRT  
 <213> Homo sapiens

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 50 55 60  
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 His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu  
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 Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln  
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 Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys  
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 Pro Pro Leu Asp Pro Gln Glu Leu Asp Ile Leu Lys Thr Val Lys Glu  
 385 390 395 400  
 Ile Thr Gly Leu Ser  
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35 40 45  
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50 55 60  
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
65 70 75 80  
Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu  
85 90 95  
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225 230 235 240  
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290 295 300  
Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln  
305 310 315 320  
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Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu  
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Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys  
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Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp  
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555 560 565  
Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp  
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685 690 695 700  
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705 710 715 720  
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Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile  
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755 760 765 770  
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<212> PRT  
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Thr Ile Gln Glu Val Ala Gly Tyr Val Leu Ile Ala Leu Asn Thr Val  
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115 120  
Lys Thr Gly Leu Lys Glu Leu Pro Met Arg Asn Leu Gln Glu Ile Leu  
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His Gly Ala Val Arg Phe Ser Asn Asn Pro Ala Leu Cys Asn Val Glu  
145 150 155 160  
Ser Ile Gln Trp Arg Asp Ile Val Ser Ser Asp Phe Leu Ser Asn Met  
165 170 175  
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Ser Cys Pro Asn Gly Ser Cys Trp Gly Ala Gly Glu Glu Asn Cys Gln  
195 200 205  
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210 215 220  
Gly Lys Ser Pro Ser Asp Cys Cys His Asn Gln Cys Ala Ala Gly Cys  
225 230 235  
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Glu Ala Thr Cys Lys Asp Thr Cys Pro Leu Met Leu Tyr Asn Pro  
255 260 265  
Thr Thr Tyr Gln Met Asp Val Asn Pro Glu Gly Lys Tyr Ser Phe Gly  
270 275 280 285  
Ala Thr Cys Val Lys Lys Cys Pro Arg Asn Tyr Val Val Thr Asp His  
290 295 300  
Gly Ser Cys Val Arg Ala Cys Gly Ala Asp Ser Tyr Glu Met Glu Glu  
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Asp Gly Val Arg Lys Cys Lys Lys Cys Glu Gly Pro Cys Arg Lys Val  
325 330 335  
Cys Asn Gly Ile Gly Ile Gly Glu Phe Lys Asp Ser Leu Ser Ile Asn  
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Ala Thr Asn Ile Lys His Phe Lys Asn Cys Thr Ser Ile Ser Gly Asp  
355 360 365  
Leu His Ile Leu Pro Val Ala Phe Arg Gly Asp Ser Phe Thr His Thr  
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Ile Thr Gly Leu Ser  
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<213> Homo sapiens

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Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
50 55 60  
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
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Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
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<212> DNA  
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 Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
 35 40 45  
 Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
 50 55 60  
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
 65 70 75 80  
 Met Arg Cys Gly Gly Cys Ser Asn Asp Gln Gly Leu Glu Cys Val Pro  
 85 90 95  
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His  
 100 105 110  
 Gln Gly Gln His Ile Gly Glu Met Ser His Gln His Asn Lys Cys  
 115 120 125  
 Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly  
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 Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr  
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 <212> DNA  
 <213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

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 Gly Pro Glu Thr Leu Cys Gly Ala Glu Leu Val Asp Ala Leu Gln Phe  
 50 55 60  
 Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn Lys Pro Thr Gly Tyr Gly  
 65 70 75 80  
 Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly Ile Val Asp Glu Cys Cys  
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 Phe Arg Ser Cys Asp Leu Arg Arg Leu Met Tyr Cys Ala Pro Leu  
 100 105 110  
 Lys Pro Ala Lys Ser Ala Arg Ser Val Arg Ala Gln Arg His Thr Asp  
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Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu  
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		145			150					155					160
Leu	Ser	Pro	Leu	Met	Ser	Arg	Ser	Gly	Cys	Lys	Val	Gly	Asp	Ser	Ser
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Gly	Thr	Ala	Ala	Ala	His	Lys	Val	Leu	Pro	Arg	Gly	Leu	Ser	Pro	Ala
			180					185					190		
Arg	Gln	Leu	Leu	Leu	Pro	Ala	Ser	Glu	Ser	Pro	His	Trp	Ser	Gly	Ala
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Pro	Pro	Gly	Ala	Ala	Ala	Gly	Gly	Val	Ala	Leu	Val	Pro	Lys	Glu	Asp
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Ser	Arg	Phe	Ser	Ala	Pro	Arg	Val	Ala	Leu	Val	Glu	Gln	Asp	Ala	Pro
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Met	Ala	Pro	Gly	Arg	Ser	Pro	Leu	Ala	Thr	Thr	Val	Met	Asp	Phe	Ile
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His	Val	Pro	Ile	Leu	Pro	Asn	His	Ala	Leu	Leu	Ala	Ala	Arg	Thr	
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Arg	Gln	Leu	Leu	Glu	Asp	Glu	Ser	Tyr	Asp	Gly	Ala	Gly	Ala	Ala	
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Pro	Arg	Ser	Tyr	Leu	Val	Ala	Gly	Ala	Asn	Pro	Ala	Ala	Phe	Pro	Asp
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Ser	Ser	Ala	Ser	Ser	Ser	Gly	Ser	Thr	Leu	Glu	Cys	Ile	Leu	Tyr	Lys
		450				455				460					
Ala	Glu	Gly	Ala	Pro	Pro	Gln	Gln	Gly	Pro	Phe	Ala	Pro	Pro	Pro	Cys
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Lys	Ala	Pro	Gly	Ala	Ser	Gly	Cys	Leu	Leu	Pro	Arg	Asp	Gly	Leu	Pro
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Ser	Thr	Ser	Ala	Ser	Ala	Ala	Ala	Ala	Gly	Ala	Ala	Pro	Ala	Leu	Tyr
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Val	Leu	Lys	Glu	Gly	Leu	Pro	Gln	Val	Tyr	Pro	Pro	Tyr	Leu	Asn	Tyr
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690 695 700  
Asn Thr Lys Pro Asp Thr Ser Ser Leu Leu Thr Ser Leu Asn Gln  
705 710 715  
Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu  
720 725 730  
Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln  
735 740 745  
Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr  
750 755 760  
Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu  
765 770 775  
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780 785 790 795  
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835 840 845  
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850 855 860  
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865 870 875  
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880 885 890 895  
Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val  
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<213> Homo sapiens

<400> 64

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 65 70 75  
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 Pro Glu Ala Phe Gln Asn Leu Pro Asn Leu Gln Tyr Leu Leu Ile Ser  
 115 120 125  
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 130 135 140  
 Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile His Thr Ile  
 145 150 155  
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 180 185 190  
 Thr Gln Leu Asp Ala Val Asn Leu Ser Asp Asn Asn Asn Leu Glu Glu  
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 225 230 235  
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 Thr Leu Glu Lys Leu Val Ala Leu Met Glu Ala Ser Leu Thr Tyr Pro  
 255 260 265  
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 320 325 330  
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Ala Ile Asp Trp Gln Thr Gly Ala Gly Cys Asp Ala Ala Gly Phe Phe  
435 440 445  
Thr Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Ala Ile Thr  
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Val Gln Leu Arg His Ala Ala Ser Val Met Val Met Gly Trp Ile Phe  
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Lys Val Ser Ile Cys Leu Pro Met Asp Ile Asp Ser Pro Leu Ser Gln  
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Ile Cys Gly Cys Tyr Ile His Ile Tyr Leu Thr Val Arg Asn Pro Asn  
545 550 555  
Ile Val Ser Ser Ser Asp Thr Arg Ile Ala Lys Arg Met Ala Met  
565 570 575  
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Ser Ser Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly  
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Asp Lys Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr  
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Cys Arg Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val  
115 120 125  
Arg Asn Asp Arg Asn Lys Lys Lys Lys Glu Val Pro Lys Pro Glu Cys  
130 135 140  
Ser Glu Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys  
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Lys Tyr Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile  
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Ser Asp Gly Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe  
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290 295 300  
Ile Cys Gly Asp Arg Gln Asp Leu Gln Pro Asp Arg Val Asp Met  
305 310 315 320  
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Arg Pro Ser Arg Pro His Met Phe Pro Lys Met Leu Met Lys Ile Thr  
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360 365 370  
Lys Met Glu Ile Pro Gly Ser Met Pro Pro Leu Ile Gln Glu Met Leu  
375 380 385  
Glu Asn Ser Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly

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<213> MUS musculus

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35 40 45  
His Ser Ser Asn Ser Asp Pro Ala Thr Arg Pro Gly Asp Ser Thr  
50 55 60  
Ser Ser Pro Val Gln Ser Ser Thr Ser Ser Pro Ala Thr Arg Ala Pro  
65 70 75 80  
Glu Asp Ser Thr Ser Thr Ala Val Leu Ser Gly Thr Ser Ser Pro Ala  
85 90 95  
Thr Thr Ala Pro Val Asn Ser Ala Ser Pro Val Ala His Gly Asp  
100 105 110  
Thr Ser Ser Pro Ala Thr Ser Pro Lys Asp Ser Asn Ser Ser Pro  
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130 135 140  
Ser Thr Ser Ser Pro Val Val His Gly Gly Thr Ser Ser Pro Ala Thr  
145 150 155 160  
Ser Pro Pro Gly Asp Ser Thr Ser Ser Pro Asp His Ser Ser Thr Ser  
165 170 175  
Ser Pro Ala Thr Arg Ala Pro Glu Asp Ser Thr Ser Thr Ala Val Leu  
180 185 190  
Ser Gly Thr Ser Ser Pro Ala Thr Thr Ala Pro Val Asp Ser Thr Ser  
195 200 205  
Ser Pro Val Ala His Asp Asp Thr Ser Ser Pro Ala Thr Ser Leu Ser  
210 215 220  
Glu Asp Ser Ala Ser Ser Pro Val Ala His Gly Gly Thr Ser Ser Pro  
225 230 235 240  
Ala Thr Ser Pro Leu Arg Asp Ser Thr Ser Ser Pro Val His Ser Ser  
245 250 255  
Ala Ser Ile Gln Asn Ile Lys Thr Thr Ser Asp Leu Ala Ser Thr Pro  
260 265 270  
Asp His Asn Gly Thr Ser Val Thr Thr Ser Ser Ala Leu Gly Ser  
275 280 285  
Ala Thr Ser Pro Asp His Ser Gly Thr Ser Thr Thr Thr Asn Ser Ser  
290 295 300  
Glu Ser Val Leu Ala Thr Thr Pro Val Tyr Ser Ser Met Pro Phe Ser  
305 310 315 320  
Thr Thr Lys Val Thr Ser Gly Ser Ala Ile Ile Pro Asp His Asn Gly  
325 330 335  
Ser Ser Val Leu Pro Thr Ser Ser Val Leu Gly Ser Ala Thr Ser Leu  
340 345 350  
Val Tyr Asn Thr Ser Ala Ile Ala Thr Thr pro Val Ser Gly Thr  
355 360 365  
Gln Pro Ser Val Pro Ser Gln Tyr Pro Val Ser Pro Thr Met Ala Thr  
370 375 380  
Thr Ser Ser His Ser Thr Ile Ala Ser Ser Tyr Tyr Ser Thr Val  
385 390 395 400  
Pro Phe Ser Thr Phe Ser Ser Asn Ser Ser Pro Gln Leu Ser Val Gly  
405 410 415  
Val Ser Phe Phe Phe Leu Phe Phe Tyr Ile Gln Asn His Pro Phe Asn  
420 425 430 435  
Ser Ser Leu Glu Asp Pro Ser Ser Asn Tyr Tyr Gln Glu Leu Lys Arg  
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Asn Ile Ser Gly Leu Phe Leu Gln Ile Phe Asn Gly Asp Phe Leu Gly  
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 Glu Val Lys Val Asn Glu Met Gln Phe Pro Pro Ser Ala Gln Ser Arg  
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 Pro Gly Val Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Ile  
 530 540  
 Leu Val Ala Leu Ala Ile Val Tyr Phe Leu Ala Leu Ala Val Cys Gln  
 545 555 560  
 Cys Arg Arg Lys Ser Tyr Gly Gln Leu Asp Ile Phe Pro Thr Gln Asp  
 565 570 575  
 Thr Tyr His Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg  
 580 585 590  
 Tyr Val Pro Pro Gly Ser Thr Lys Arg Gln Pro Tyr Glu Glu Val Ser  
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 His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala  
 65 70 75 80  
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 85 90 95  
 Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp  
 100 105 110  
 Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val  
 115 120 125  
 Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Ser His Arg Gln  
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<212> DNA  
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<212> PRT  
<213> Homo sapiens

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Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp  
65 70 75 80  
His Arg Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val  
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<210> 74  
<211> 1602  
<212> DNA  
<213> Mus musculus

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ggattgttaa tgtttgcatt tcttcagggt ctttagtctg ttgttcttga aaactaaga 6360
tacatcctgt gtttgcttgg cttactgaag aaagtagaag aagataaact gataataata 6420
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<210> 79  
<211> 1142  
<212> PRT  
<213> Homo sapiens

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<400> 79
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20      25      30
Ser Pro Leu Gln Ile Pro Gln Ser Ser Pro Glu Ser Asp Thr Leu
35      40      45
Tyr Pro Leu Gln Ser Pro Gln Ser Arg Ser Glu Gly Glu Asp Ser Ser
50      55      60
Asp Pro Leu Gln Arg Pro Pro Glu Gly Lys Asp Ser Gln Ser Pro Leu
65      70      75
Gln Ile Pro Gln Ser Ser Pro Glu Gly Lys Asp Thr Gln Ser Pro Leu
85      90      95
Gln Asn Ser Gln Ser Ser Pro Glu Gly Lys Asp Ser Leu Ser Pro Leu
100     105     110
Glu Ile Ser Gln Ser Pro Pro Glu Gly Glu Asp Val Gln Ser Pro Leu
115     120     125
Gln Asn Pro Ala Ser Ser Phe Ser Ser Ala Leu Leu Ser Ile Phe
130     135     140
Gln Ser Ser Pro Glu Ser Ile Gln Ser Pro Phe Glu Gly Phe Pro Gln
145     150     155
Ser Val Leu Gln Ile Pro Val Ser Ala Ala Ser Ser Ser Thr Leu Val
160     165     170
Ser Ile Phe Gln Ser Ser Pro Glu Ser Thr Gln Ser Pro Phe Glu Gly
175     180     185
Phe Pro Gln Ser Pro Leu Gln Ile Pro Val Ser Arg Ser Phe Ser Ser
190     195     200
Thr Leu Leu Ser Ile Phe Gln Ser Ser Pro Glu Arg Ser Gln Arg Thr
205     210     215
Ser Glu Gly Phe Ala Gln Ser Pro Leu Gln Ile Pro Val Ser Ser Ser
220     225     230
Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu Arg Thr
235     240     245
Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Val
250     255     260
Ser Arg Ser Phe Ser Ser Thr Leu Leu Ser Ile Phe Gln Ser Ser Pro
265     270     275
Glu Arg Thr Gln Ser Thr Phe Glu Gly Phe Ala Gln Ser Pro Leu Gln
280     285     290
Ile Pro Val Ser Ser Ser Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln
295     300     305
Ser Ser Pro Glu Arg Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser
310     315     320
Leu Leu Gln Ile Pro Met Thr Ser Ser Phe Ser Ser Thr Leu Leu Ser
325     330     335
Ile Phe Gln Ser Ser Pro Glu Ser Ala Gln Ser Thr Phe Glu Gly Phe
340     345     350
Pro Gln Ser Pro Leu Gln Ile Pro Gly Ser Pro Phe Ser Ser Thr
355     360     365
Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu Arg Thr His Ser Thr Phe
370     375     380
Glu Leu Ser Leu Phe Gln Ser Ser Pro Glu Arg Thr His Ser Thr Phe
385     390     395
Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Met Thr Ser Ser Phe
400

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 Ser Ser Phe Ser Tyr Thr Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu  
 450 455 460  
 Arg Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile  
 465 470 475 480  
 Pro Val Ser Ser Ser Ser Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln  
 485 490 495  
 Ser Ser Pro Glu Cys Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser  
 500 505 510  
 Pro Leu Gln Ile Pro Gln Ser Pro Glu Gly Glu Asn Thr His Ser  
 515 520 525  
 Pro Leu Gln Ile Val Pro Ser Ser Pro Glu Trp Glu Asp Ser Leu Ser  
 530 535 540  
 Pro His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Leu Ser  
 545 550 555 560  
 Pro His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Leu Ser  
 565 570 575  
 Pro His Tyr Phe Pro Gln Ser Pro Gln Gly Glu Asp Ser Leu Ser Pro  
 580 585 590  
 His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Met Ser Pro  
 595 600 605  
 Leu Tyr Phe Pro Gln Ser Pro Leu Gln Gly Glu Glu Phe Gln Ser Ser  
 610 615 620  
 Leu Gln Ser Pro Val Ser Ile Cys Ser Ser Ser Thr Pro Ser Ser Leu  
 625 630 635 640  
 Pro Gln Ser Phe Pro Glu Ser Ser Gln Ser Pro Pro Glu Gly Pro Val  
 645 650 655  
 Gln Ser Pro Leu His Ser Pro Gln Ser Pro Pro Glu Gly Met His Ser  
 660 665 670  
 Gln Ser Pro Leu Gln Ser Pro Glu Ser Ala Pro Glu Gly Glu Asp Ser  
 675 680 685  
 Leu Ser Pro Leu Gln Ile Pro Gln Ser Pro Leu Glu Gly Glu Asp Ser  
 690 695 700  
 Leu Ser Ser Leu His Phe Pro Gln Ser Pro Pro Glu Trp Glu Asp Ser  
 705 710 715 720  
 Leu Ser Pro Leu His Phe Pro Gln Phe Pro Pro Gln Gly Glu Asp Phe  
 725 730 735  
 Gln Ser Ser Leu Gln Ser Pro Val Ser Ile Cys Ser Ser Ser Thr Ser  
 740 745 750  
 Leu Ser Leu Pro Gln Ser Phe Pro Glu Ser Pro Gln Ser Pro Pro Glu  
 755 760 765  
 Gly Pro Ala Gln Ser Pro Leu Gln Arg Pro Val Ser Ser Phe Phe Ser  
 770 775 780  
 Tyr Thr Leu Ala Ser Leu Gln Ser Ser His Glu Ser Pro Gln Ser  
 785 790 795 800  
 Pro Pro Glu Gly Pro Ala Gln Ser Pro Leu Gln Ser Pro Val Ser Ser  
 805 810 815  
 Phe Pro Ser Ser Thr Ser Ser Ser Leu Ser Gln Ser Ser Pro Val Ser  
 820 825 830  
 Ser Phe Pro Ser Ser Thr Ser Ser Ser Leu Ser Lys Ser Pro Glu  
 835 840 845  
 Ser Pro Leu Gln Ser Pro Val Ile Ser Phe Ser Ser Ser Thr Ser Leu  
 850 855 860  
 Ser Pro Phe Ser Glu Glu Ser Ser Ser Pro Val Asp Glu Tyr Thr Ser  
 865 870 875 880  
 Ser Ser Asp Thr Leu Leu Glu Ser Asp Ser Leu Thr Asp Ser Glu Ser  
 885 890 895  
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 900 905 910  
 Asp Glu Leu Ala Arg Phe Leu Leu Lys Tyr Gln Val Lys Gln Pro  
 915 920 925  
 Ile Thr Lys Ala Glu Met Leu Thr Asn Val Ile Ser Arg Tyr Thr Gly  
 930 935 940  
 Tyr Phe Pro Val Ile Phe Arg Lys Ala Arg Glu Phe Ile Glu Ile Leu  
 945 950 955 960

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Gly Met Ser Gln Asn Arg Leu Leu Ile Leu Ser Ile Ile Phe  
995 1000 1005  
Ile Lys Gly Thr Tyr Ala Ser Glu Val Ile Trp Asp Val Leu Ser  
1010 1015 1020  
Gly Ile Gly Val Arg Ala Gly Arg Glu His Phe Ala Phe Gly Glu Pro  
1025 1030 1035 1040  
Arg Glu Leu Leu Thr Lys Val Trp Val Gln Glu His Tyr Leu Glu Tyr  
1045 1050 1055  
Arg Glu Val Pro Asn Ser Ser Pro Pro Arg Tyr Glu Phe Leu Trp Gly  
1060 1065 1070  
Pro Arg Ala His Ser Glu Val Ile Lys Arg Lys Val Val Glu Phe Leu  
1075 1080 1085  
Ala Met Leu Lys Asn Thr Val Pro Ile Thr Phe Pro Ser Ser Tyr Lys  
1090 1095 1100  
Asp Ala Leu Lys Asp Val Glu Glu Arg Ala Gln Ala Ile Ile Asp Thr  
1105 1110 1115 1120  
Thr Asp Asp Ser Thr Ala Thr Glu Ser Ala Ser Ser Ser Val Met Ser  
1125 1130 1135  
Pro Ser Phe Ser Ser Glu  
1140

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<211> 1004  
<212> DNA  
<213> Homo sapiens

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gtggtggcaa cagagatggc agcgagctg gagtgttagg agggcgccct gaggcgtagg 180  
agtggggctg gagcagtaag atggcgcca gagcggttt tctggcattg tctgccagc 240  
tgctccaagc caggctgatg aaggaggagt cccctgtgtt gagctggagg ttggagcctg 300  
aagacggac agctctgtgc ttcattctt gaggtgtgg cagccacggt gatggagac 360  
gcagctcaac aggagcaata ggagagatg gagtctact gtgcagcca gtaggtctc 420  
gatctctga cctctgtatc cgcccgctt ggccttccaa agtgccgaga ttacgcgat 480  
gtgcattttg taagcacttt ggagccacta tcaaatgctg tgaagagaaa tgaaccagaa 540  
tgtatcatta tcttctgtct gcaggagcgc gctcctttca ggaattcagt cacatcttcc 600  
tgctttgtcc agaaccattt gaccaagctc ctgaaagatg taagtttact acgcatagac 660  
ttttaacctt caaccaatgt atttactgaa aataacaagt gttgtaaatt ccctgagtgt 720  
tattctactt gtattaaaaa gtaataatc ataataatc aaatctgagg gatcattgcc 780  
agagattggt ggggagggaa atgttatcaa cggtttcatt gaaattaaat ccaaaaagt 840  
atttctcag aaaaatcaaa taaagtttgc atgtttttta ttcttaaaac attttaaaaa 900  
cactgtaga atgatgtaaa tagggactgt gcagtatttc tgacatatat tataaaaata 960  
ttaaaaagtc aatcagtatt caacatcttt tactataaaa agcc 1004

<210> 81  
<211> 43  
<212> PRT  
<213> Homo sapiens

<400> 81  
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20 25 30  
Pro Glu Asp Gly Thr Ala Leu Cys Phe Ile Phe  
35 40

<210> 82  
<211> 646  
<212> DNA  
<213> Homo sapiens

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cctatgcggc ccgagcagtt cagtgtatga gtggaaccag caacacctga agaaggggaa 180  
ccagcaactc aacgtcagga tctctcagct gctcaggagg gagaggatga gggagcatct 240  
gcaggtcaag ggcgcaagcc tgaagctgat agccaggaac aggggtcacc acagactggg 300  
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ttctcccaat aaagctttac agccttctgc aaagaaaaa aaaaaa 646

<210> 83  
<211> 138  
<212> PRT  
<213> Homo sapiens

<400> 83  
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20 25 30  
Asp Glu Val Glu Pro Ala Thr Pro Glu Gly Glu Pro Ala Thr Gln  
35 40 45  
Arg Gln Asp Pro Ala Ala Ala Gln Glu Gly Glu Asp Glu Gly Ala Ser  
50 55 60  
Ala Gly Gln Gly Pro Lys Pro Glu Ala Asp Ser Gln Glu Gln Gly His  
65 70 75 80  
Pro Gln Thr Gly Cys Glu Cys Glu Asp Gly Pro Asp Gly Gln Glu Met  
85 90 95  
Asp Pro Pro Asn Pro Glu Glu Val Lys Thr Pro Glu Glu Glu Met Arg  
100 105 110  
Ser His Tyr Val Ala Gln Thr Gly Ile Leu Trp Leu Leu Met Asn Asn  
115 120 125  
Cys Phe Leu Asn Leu Ser Pro Arg Lys Pro  
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<210> 84  
<211> 766  
<212> DNA  
<213> Homo sapiens

<400> 84  
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accacaggtt ggtgtctaaa taccagagaa gatccaaaag gccttcgatg atattgccaa 180  
atattctctt aaggaagagt gggaaaagat gaaagcctcg gagaaaaatc tctatgtgta 240  
tatgaagaga aagtatgagg ctatgactaa actaggtttc aaggccaccc tcccaccttt 300  
catgtgtaat aaacgggccg aagacttcca ggggaatgat ttgataaatg acccetaaccg 360  
tgggaatcag gttgaacgtc ctccagatgac ttctggcagg ctccagggaa tctcccggaa 420  
gatcatgcc tgaagtcag cagagggaag aaatgattcg gaggaagtgc cagaagcatt 480  
tgcccacaaa aatgtgggga agagactgtg ccccccggga aaaccaaata cctctgagaa 540  
gttccacgag agatctggac ccaaaagggg ggaacctgac tgaaccaca gactgcgtga 600  
gagaaaacag ctggtgattt atgaagagat cagcgaccct gaggaagatg acgagtaact 660  
ccctcagagg atacacaca tgcccatgat gagaagcaga acgttgtgac ctttcacgaa 720  
catgggcatg gctcggacc cctcgtcatc aggtgcatag caatgtg 766

<210> 85  
<211> 188  
<212> PRT  
<213> Homo sapiens

<400> 85  
Met Asn Gly Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln  
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Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe  
20 25 30

http://www.uspto.gov/patent

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50 55 60  
Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln  
65 70 75  
Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg  
85 90 95  
Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met  
100 105 110  
Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu  
115 120 125  
Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys  
130 135 140  
Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly  
145 150 155  
Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile  
160 165 170 175  
Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu  
180 185

<210> 86  
<211> 2974  
<212> DNA  
<213> Homo sapiens

<400> 86  
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tgtgaacctg aggtcagaaa cacaaacct acctgtgtgg taaattgtca gagctccca 1740  
gtcagtccca ggctcagct gtccaatggc aacaggacc tcactctatt caatgtcaca 1800  
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tcgtcttacc ctggggagc gaacctcaac ctctctgccc actcgccctc taaccctatc 1980  
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<210> 87  
 <211> 702  
 <212> PRT  
 <213> Homo sapiens

<400> 87  
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 Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr  
 20 25 30  
 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly  
 35 40 45  
 Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly  
 50 55 60  
 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile  
 65 70 75 80  
 Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser  
 85 90 95  
 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile  
 100 105 110  
 Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp  
 115 120 125  
 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu  
 130 135 140  
 Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys  
 145 150 155  
 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr  
 160 165 170  
 Leu Trp Trp Val Asn Asn Gln Ser Leu Val Ser Pro Arg Leu Gln  
 175 180 185  
 Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn  
 190 195 200  
 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg  
 205 210 215  
 Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro  
 220 225 230  
 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn  
 235 240 245  
 Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe  
 250 255 260  
 Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn  
 265 270 275  
 Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser  
 280 285 290  
 Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala  
 295 300 305  
 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu  
 310 315 320  
 Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr  
 325 330 335  
 Thr Tyr Leu Trp Trp Val Asn Asn Ser Leu Leu Pro Val Ser Pro Arg  
 340 345 350  
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 355 360 365  
 Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser  
 370 375 380  
 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp  
 385 390 395  
 Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn  
 400 405 410 415



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 420 425 430  
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 450 455 460  
 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn  
 465 470 475 480  
 Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val  
 485 490 495  
 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro  
 500 505 510  
 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln  
 515 520 525  
 Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Ser Leu Pro Val Ser  
 530 535 540  
 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn  
 545 550 555 560  
 Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser  
 565 570 575  
 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly  
 580 585 590  
 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly  
 595 600 605  
 Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln  
 610 615 620  
 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu  
 625 630 635 640  
 Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe  
 645 650 655  
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<210> 93  
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 <212> PRT  
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<400> 93  
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 Phe Gln Ala Arg Leu Thr Arg Ser Asn Ser Lys Cys Gln Gly Gln Leu  
 35 40 45  
 Glu Val Tyr Leu Lys Asp Gly Trp His Met Val Cys Ser Gln Ser Trp  
 50 55 60  
 Gly Arg Ser Ser Lys Gln Trp Glu Asp Pro Ser Gln Ala Ser Lys Val  
 65 70 75 80  
 Cys Gln Arg Leu Asn Cys Gly Val Pro Leu Ser Leu Gly Pro Phe Leu  
 85 90 95  
 Val Thr Tyr Thr Pro Gln Ser Ser Ile Ile Cys Tyr Gly Gln Leu Gly  
 100 105  
 Ser Phe Ser Asn Cys Ser His Ser Arg Asn Asp Met Cys His Ser Leu  
 115 120 125  
 Gly Leu Thr Cys Leu Glu Pro Gln Lys Thr Thr Pro Pro Thr Thr Arg  
 130 135 140  
 Pro Pro Pro Thr Thr Thr Pro Glu Pro Thr Ala Pro Pro Arg Leu Gln  
 145 150 155 160  
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 Tyr Ser Gly Ser Leu Gly Gly Thr Ile Ser Tyr Glu Ala Gln Asp Lys  
 180 185 190  
 Thr Gln Asp Leu Glu Asn Phe Leu Cys Asn Asn Leu Gln Cys Gly Ser  
 195 200 205  
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 Gly Glu Pro Arg Glu His Gln Pro Leu Pro Ile Gln Trp Lys Ile Gln  
 225 230 235 240  
 Asn Ser Ser Cys Thr Ser Leu Glu His Cys Phe Arg Lys Ile Lys Pro  
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 260 265 270  
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 275 280 285  
 Val Glu Val Arg Gln Gly Ala Gln Trp Ala Ala Leu Cys Asp Ser Ser  
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 Ser Ala Arg Ser Ser Leu Arg Trp Glu Glu Val Cys Arg Glu Gln Gln  
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370 375 380  
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Ala Tyr Lys Lys Leu Val Lys Lys Phe Arg Gln Lys Lys Gln Arg Gln  
405 410 415  
Trp Ile Gly Pro Thr Gly Met Asn Gln Asn Met Ser Phe His Arg Asn  
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<210> 94  
<211> 1586  
<212> DNA  
<213> Homo sapiens

<400> 94  
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<210> 95  
<211> 420  
<212> PRT  
<213> Homo sapiens

<400> 95  
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Lys Val Gln Asn Ile His Pro Val Glu Ser Ala Lys Ile Glu Pro Pro  
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 245 250 255  
 Ser Asp Gly Phe Leu Asp Glu Gln Glu Leu Glu Ala Leu Phe Thr Lys  
 260 265 270  
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 Ala Thr Glu Lys Lys Glu Phe Leu Glu Pro Asp Ser Trp Glu Thr Leu  
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 340 345 350  
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 355 360 365  
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 370 375 380  
 Gln Lys Leu Glu Tyr His Gln Val Ile Gln Gln Met Glu Gln Lys Lys  
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 <212> DNA  
 <213> Homo sapiens

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 taactctgtg ttctctgttc gcaactgcac catcactgcc aatgctgagt gtgcctgtcg 420  
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cacc

<210> 97  
<211> 260  
<212> PRT  
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Cys Ile Pro Gly Val Ser Phe Ser Pro Asp His His Thr Arg Pro His  
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Cys Glu Ser Cys Arg His Cys Asn Ser Gly Leu Leu Val Arg Asn Cys  
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Arg Asp Lys Glu Cys Thr Glu Cys Asp Pro Leu Pro Asn Pro Ser Leu  
115 120 125  
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130 135 140  
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145 150 155 160  
Gln Thr Leu Ala Asp Phe Arg Gln Leu Pro Ala Arg Thr Leu Ser Thr  
165 170 175  
His Trp Pro Pro Gln Arg Ser Leu Cys Ser Ser Asp Phe Ile Arg Ile  
180 185 190  
Leu Val Ile Phe Ser Gly Met Phe Leu Val Phe Thr Leu Ala Gly Ala  
195 200 205  
Leu Phe Leu His Gln Arg Arg Lys Tyr Arg Ser Asn Lys Gly Glu Ser  
210 215 220  
Pro Val Glu Pro Ala Glu Pro Cys Arg Tyr Ser Cys Pro Arg Glu Glu  
225 230 235 240  
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245 250 255  
Ala Cys Ser Pro  
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<210> 98  
<211> 1514  
<212> DNA  
<213> Homo sapiens

<400> 98  
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tcaagggagt tccgggcatc ctttcacaaa ggacttgata gtgctgtgga agtctgtgtt 300  
gtatatggga attactccca gcagcttcag gttacttcaa aaacgggggt caactctgat 360  
gggaaatttg gcaatgaatc agtgacattc tacctccaga atttgatgt taacaaaca 420  
gatatttact tctgcaaaat tgaagtattg tatctctctc ttactctaga caatgagaag 480  
agcaatggaa ccattatcca tgtgaaaggg aaacaccttt gtccaagtcc cctatttccc 540  
agcccttttg ggtgctgttg gtggttggtg gaggctggc ttgctatagc 600  
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cacagtgact acatgaacat gactcccgcg ccccggggc ccaccggcaa gcattaccag 720

http://www.uspto.gov/patent

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<211> 220  
<212> PRT  
<213> Homo sapiens

<400> 99  
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Thr Gly Asn Lys Ile Leu Val Lys Gln Ser Pro Met Leu Val Ala Tyr  
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Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser  
35 40 45  
Arg Gly Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu  
50 55 60  
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser  
65 70 75 80  
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr  
85 90 95  
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys  
100 105 110  
Lys Ile Glu Val Met Tyr Pro Pro Tyr Leu Asp Asn Glu Lys Ser  
115 120 125  
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro  
130 135 140  
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly  
145 150 155 160  
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile  
165 170 175  
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met  
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Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro  
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Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser  
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<210> 100  
<211> 672  
<212> DNA  
<213> Homo sapiens

<400> 100  
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<212> PRT  
<213> Homo sapiens

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Val Phe Cys Lys Ala Met His Val Ala Gln Pro Ala Val Leu Ala  
35 40 45  
Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly  
50 55 60  
Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln  
65 70 75 80  
Val Thr Glu Val Cys Ala Ala Thr Tyr Met Thr Gly Asn Glu Leu Thr  
85 90 95  
Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val  
100 105 110  
Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile  
115 120 125  
Cys Lys Val Glu Leu Met Tyr Pro Pro Tyr Tyr Leu Gly Ile Gly  
130 135 140  
Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser  
145 150 155 160  
Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe  
165 170 175  
Tyr Ser Phe Leu Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys  
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Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu  
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<210> 102  
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<212> DNA  
<213> Homo sapiens

<400> 102  
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gatacaattt ttattaaagt catagtggat acttcggatc tgcctgatcc ctgataagta 1920  
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aaaagaacca tgatttttct tccttaactt tgaacaccaa aaaaacacac acacacacac 2280  
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<212> PRT  
<213> Homo sapiens

<400> 103  
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35 40 45  
Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys  
50 55 60  
Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu  
65 70 75 80  
Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val  
85 90 95  
Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala  
100 105 110  
Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu  
115 120 125  
Met Leu Gly His Leu Val His Leu Lys Asn Asp Cys His Phe Glu Glu  
130 135 140  
Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys Asp  
145 150 155  
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160 165 170 175  
Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His Glu  
180 185 190  
Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser  
195 200 205  
Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys  
210 215 220  
Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe  
225 230 235 240  
Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val  
245 250 255  
Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys  
260 265 270  
Val Ser Leu Leu Gln Asn Glu Val Glu Lys Asn Lys Ser Ile Gln  
275 280 285  
Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln  
290 295 300  
Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg  
305 310 315 320  
Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile  
325 330 335  
Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser  
340 345 350  
Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys  
355 360 365  
Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu  
370 375 380  
Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp

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420 425 430  
Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr  
435 440 445  
Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met  
450 455 460  
Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu  
465 470 475 480  
Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met  
485 490 495  
Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys  
500 505 510  
Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn  
515 520 525  
Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn  
530 535 540  
Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp  
545 550 555 560  
Thr Ser Asp Leu Pro Asp Pro  
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<211> 1874  
<212> DNA  
<213> Homo sapiens

<400> 104  
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caggaatcac aatccacga aatccagatt gcccaaatc tgaggacaag aacttcccc 180  
ggactgtgat ggtcaacctg accgtcaatac caataccaat cccaaaaggt 240  
ctcagatatt ctacaaccga tccacctcac ctggaatct ccaccgcaat gaggaccctg 300  
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ctccccaagc cagttagact atggagagcc gacccagccc ctcaggaaac ctcatcctc 600  
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agcttcagag gcaacacttg gccaaagatc gagaactgaa ttactcttcc ctcttccaa 720  
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<211> 155  
<212> PRT  
<213> Homo sapiens

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Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn  
35 40 45  
Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser  
50 55 60  
Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu  
65 70 75  
Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His  
85 90 95  
Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser  
100 105 110  
Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Glu Pro Pro His  
115 120 125  
Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys  
130 135 140  
Thr Cys Val Thr Pro Ile Val His His Val Ala  
145 150 155

<210> 106  
<211> 3120  
<212> DNA  
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 gccgaggaca cgtaaacga acaggatggg ccgggcacgg tggctcacg ctgtaatccc 3060  
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 <211> 866  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp Ser Trp Ile His  
 50 55 60  
 Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp Leu Gln Ile Gln Leu  
 65 70 75 80  
 His Phe Ala His His Thr Gln Gln Gly Asp Leu Phe Pro Val Ala His Ile  
 85 90 95  
 Glu Trp Thr Leu Gln Thr Asp Ala Ser Ile Leu Tyr Leu Glu Gly Ala  
 100 105 110  
 Glu Leu Ser Val Leu Gln Leu Asn Thr Asn Glu Arg Leu Cys Val Arg  
 115 120 125  
 Phe Glu Phe Leu Ser Lys Leu Arg His His His Arg Trp Arg Phe  
 130 135 140  
 Thr Phe Ser His Phe Val Val Asp Pro Asp Gln Tyr Gln Val Thr  
 145 150 155  
 Val His His Leu Pro Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln  
 160 165 170  
 Ser Lys Asn Phe Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val  
 175 180 185  
 Thr Thr Pro Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr  
 190 195 200  
 Val Glu Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp  
 205 210 215  
 Asn Glu Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met  
 220 225 230 235  
 Glu Asn His Ser Cys Phe Glu His Met His His Ile Pro Ala Pro Arg  
 240 245 250 255  
 Pro Glu Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu Arg Asn  
 260 265 270  
 Leu Lys Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro Phe Phe Ser  
 275 280 285  
 Ser Cys Leu Asn Asp Cys Leu Arg His Ser Ala Thr Val Ser Cys Pro  
 290 295 300  
 Glu Met Pro Asp Thr Pro Glu Pro Ile Pro Asp Tyr Met Pro Leu Trp  
 305 310 315 320  
 Val Tyr Trp Phe Ile Thr Gly Ile Ser Ile Leu Leu Val Gly Ser Val  
 325 330 335  
 Ile Leu Leu Ile Val Cys Met Thr Trp Arg Leu Ala Gly Pro Gly Ser  
 340 345 350  
 Glu Lys Tyr Ser Asp Asp Thr Lys Tyr Thr Asp Gly Leu Pro Ala Ala  
 355 360 365  
 Asp Leu Ile Pro Pro Pro Leu Lys Pro Arg Lys Val Trp Ile Ile Tyr  
 370 375 380  
 Ser Ala Asp His Pro Leu Tyr Val Asp Val Val Leu Lys Phe Ala Gln

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 420 425 430  
 Lys Gln Glu Met Val Glu Ser Asn Ser Lys Ile Ile Val Leu Cys Ser  
 435 440 445  
 Arg Gly Thr Arg Ala Lys Trp Gln Ala Leu Leu Gly Arg Gly Ala Pro  
 450 455 460  
 Val Arg Leu Arg Cys Asp His Gly Lys Pro Val Gly Asp Leu Phe Thr  
 465 470 475 480  
 Ala Ala Met Asn Met Ile Leu Pro Asp Phe Lys Arg Pro Ala Cys Phe  
 485 490 495  
 Gly Thr Tyr Val Val Cys Tyr Phe Ser Glu Val Ser Cys Asp Gly Asp  
 500 505 510  
 Val Pro Asp Leu Phe Gly Ala Ala Pro Arg Tyr Pro Leu Met Asp Arg  
 515 520 525  
 Phe Glu Glu Val Tyr Phe Arg Ile Gln Asp Leu Glu Met Phe Gln Pro  
 530 535 540  
 Gly Arg Met His Arg Val Gly Glu Leu Ser Gly Asp Asn Tyr Leu Arg  
 545 550 555 560  
 Ser Pro Gly Gly Arg Gln Leu Arg Ala Ala Leu Asp Arg Phe Arg Asp  
 565 570 575  
 Trp Gln Val Arg Cys Pro Asp Trp Phe Glu Cys Glu Asn Leu Tyr Ser  
 580 585 590  
 Ala Asp Asp Gln Asp Ala Pro Ser Leu Asp Glu Glu Val Phe Glu Glu  
 595 600 605  
 Pro Leu Leu Pro Pro Gly Thr Ile Val Lys Arg Ala Pro Leu Val  
 610 615 620  
 Arg Glu Pro Gly Ser Gln Ala Cys Leu Ala Ile Asp Pro Leu Val Gly  
 625 630 635 640  
 Glu Glu Gly Gly Ala Ala Val Ala Lys Leu Glu Pro His Leu Gln Pro  
 645 650 655  
 Arg Gly Gln Pro Ala Pro Gln Pro Leu His Thr Leu Val Leu Ala Ala  
 660 665 670  
 Glu Glu Gly Ala Leu Val Ala Ala Val Glu Pro Gly Pro Leu Ala Asp  
 675 680 685  
 Gly Ala Ala Val Arg Leu Ala Leu Ala Gly Glu Gly Glu Ala Cys Pro  
 690 695 700  
 Leu Leu Gly Ser Pro Gly Ala Gly Arg Asn Ser Val Leu Phe Leu Pro  
 705 710 715 720  
 Val Asp Pro Glu Asp Ser Pro Leu Gly Ser Thr Pro Met Ala Ser  
 725 730 735  
 Pro Asp Leu Leu Pro Glu Asp Val Arg Glu His Leu Glu Gly Leu Met  
 740 745 750  
 Leu Ser Leu Phe Glu Gln Ser Leu Ser Cys Gln Ala Gln Gly Gly Cys  
 755 760 765  
 Ser Arg Pro Ala Met Val Leu Thr Asp Pro His Thr Pro Tyr Glu Glu  
 770 775 780  
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 785 790 795 800  
 Ser Pro Gln Pro Pro Glu Gly Leu Thr Glu Met Glu Glu Glu Glu Glu  
 805 810 815  
 Glu Glu Gln Asp Pro Gly Lys Pro Ala Leu Pro Leu Ser Pro Glu Asp  
 820 825 830  
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 <211> 578  
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 <213> Homo sapiens  
 <400> 108



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 ttggcagcagc ctggagcctt catccctaag tcaaccaccag gagagccttc cccaattctc 480  
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 <211> 128  
 <212> PRT  
 <213> Homo sapiens

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 Asn Pro Thr Ala Asp Cys Lys Thr Ala Val Asn Cys Ser Ser Asp Phe  
 35 40 45  
 Asp Ala Cys Leu Ile Thr Lys Ala Gly Leu Gln Val Tyr Asn Lys Cys  
 50 55 60  
 Trp Lys Phe Glu His Cys Asn Phe Asn Asp Val Thr Thr Arg Leu Arg  
 65 70 75  
 Glu Asn Glu Leu Thr Tyr Cys Cys Lys Lys Asp Leu Cys Asn Phe  
 80 85 90 95  
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 Leu Leu Leu Val Thr Pro Phe Leu Ala Ala Ala Trp Ser Leu His Pro  
 115 120 125

<210> 110  
 <211> 1048  
 <212> DNA  
 <213> Homo sapiens

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 agtacttata atccaatttt aaaggcaggg tcagacttga tcttcagagt ggcgcactgt 300  
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 tcatacaaat tgagaagata gaagacatgg atgacaactg ttatctgtaa ctgtctatgt 480  
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          9135          9140          9145
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          9195          9200          9205
          9210          9215          9220
          9225          9230          9235
          9240          9245          9250
          9255          9260          9265
          9270          9275          9280
          9285          9290          9295
          9300          9305          9310
          9315          9320          9325
          9330          9335          9340
          9345          9350          9355
          9360          9365          9370
          9375          9380          9385
          9390          9395          9400
          9405          9410          9415
          9420          9425          9430
          9435          9440          9445
          9450          9455          9460
          9465          9470          9475
          9480          9485          9490
          9495          9500          9505
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          9540          9545          9550
          9555          9560          9565
          
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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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50 55 60  
Gly Ser Glu Gln Pro Thr Ala Thr Trp Ser Ser Val Lys Ser Ser Ala  
65 70 75 80  
Leu Arg Gln Ile Pro Arg Cys Pro Thr Val Cys Leu Gln Asn Phe Leu  
85 90 95  
Leu Gly Leu Leu Ser Cys Leu Met Leu Gly Val Ala Val Ile Cys  
100 105 110  
Leu Gly Val Arg Tyr Leu Gln Val Ser Gln Gln Phe Gln Gly Thr  
115 120 125  
Arg Ile Trp Glu Ala Thr Asn Ser Ser Leu Gln Gln Leu Arg Glu  
130 135 140  
Lys Ile Ser Gln Leu Gly Gln Lys Glu Val Glu Gln Glu Ser Gln Lys  
145 150 155 160  
Glu Leu Ile Ser Ser Gln Asp Thr Leu Gln Glu Lys Gln Arg Thr His  
165 170 175  
Lys Asp Thr Glu Gln Gln Leu Gln Ala Cys Gln Ala Glu Ala Lys  
180 185 190  
Thr Lys Glu Asn Leu Lys Thr Glu Glu Glu Arg Arg Asp Leu Asp  
195 200 205  
Gln Arg Leu Thr Ser Thr Arg Glu Thr Leu Arg Arg Leu Ser Ser Cys  
210 215 220  
Ser Ser Asp Thr Cys Cys Pro Cys Gly Trp Ile Pro Tyr Gln Glu Arg  
225 230 235 240  
Cys Phe Tyr Ile Ser His Thr Leu Arg Ser Leu Glu Glu Ser Gln Lys  
245 250 255  
Tyr Cys Thr Ser Leu Ser Ser Lys Leu Ala Ala Phe Asp Glu Pro Ser  
260 265 270  
Lys Tyr Tyr Glu Tyr Leu Ser Asp Ala Pro Gln Val Ser Leu Pro  
275 280 285  
Ser Gly Leu Glu Glu Leu Leu Asp Arg Ser Lys Ser Tyr Trp Ile Gln  
290 295 300  
Met Ser Lys Lys Trp Arg His Asp Tyr Asp Ser Gln Ser Arg Tyr Cys  
305 310 315 320  
Asp Lys Ile Lys Lys Tyr Tyr Gln Lys Trp Lys Arg Thr Phe Ser Glu  
325 330 335  
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340 345 350  
Pro Asp Gly Ile His Leu Asn  
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<213> Mus musculus

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tcggctgagg aggctacacg ttcccgcctg cttcaggccg ctgcttccgt gcagggatgc 180  
cggaggaaagg tcgaccttgc ccttgggttc gctggagcgg gaccgcgttc cagcgccaat 240  
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gcactactcag taagcagcaa cagaggctgc tggagcaccc tgagccgcac acagctgagt 360  
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<210> 117  
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Val Phe Cys Cys Trp Phe His Cys Ser Gly Leu Leu Ser Lys Gln Gln  
35 40 45  
Gln Arg Leu Leu Glu His Pro Glu Pro His Thr Ala Glu Leu Gln Leu  
50 55 60  
Asn Leu Thr Val Pro Arg Lys Asp Pro Thr Leu Arg Trp Gly Ala Gly  
65 70 75 80  
Pro Ala Leu Gly Arg Ser Phe Thr His Gly Pro Glu Leu Glu Gly  
85 90 95  
His Leu Arg Ile His Gln Asp Gly Leu Tyr Arg Leu His Ile Gln Val  
100 105 110  
Thr Leu Ala Asn Cys Ser Ser Pro Gly Ser Thr Leu Gln His Arg Ala  
115 120 125  
Thr Leu Ala Val Gly Ile Cys Ser Pro Ala Ala His Gly Ile Ser Leu  
130 135 140  
Leu Arg Gly Arg Phe Gly Gln Asp Cys Thr Val Ala Leu Arg Leu  
145 150 155 160  
Thr Tyr Leu Val His Gly Asp Val Leu Cys Thr Asn Leu Thr Leu Pro  
165 170 175  
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180 185 190  
Ile Cys Pro  
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<211> 909  
<212> DNA  
<213> Homo sapiens

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gaaggaagcc gttttgatatt aaatgatggt tacgtatatt ggcaaacacc tgagtcgaaa 180  
accgtggtga cctaccacat ccacacagaac agctccttgg aaaaagtggg cagccgctac 240  
cggaaccgag ccctgatgtc accggccggc atgtctgggg gcgacttctc cctgcgcttg 300  
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cccgctgtca gcgcccccac cagcctctcc caggtatgag tcaacctcac gtgtacatcc 480  
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gaccaggctc tgcagaatga caccgtcttc ttgaacatgc ggggcttgta tgacgtggtc 600  
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aagatcacag agaattccagt cagtaccggc gagaaaaacg cgccacgtg gagcatcctg 780  
gctgtcctgt gcctgctgtt ggtcgtggcg gtggccatag cctgggtgtg cagggaccga 840  
tgctcccaac acagctatgc aggtgcctgg cgtgtgagtc cggagacaga gctcactggc 900  
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<210> 119  
<211> 302  
<212> PRT  
<213> Homo sapiens

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20 25 30  
Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn  
35 40 45  
Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr  
50 55 60  
Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr  
65 70 75 80  
Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt  
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 115 120 125  
 Glu Val Thr Leu His Val Ala Asn Phe Ser Val Pro Val Val Ser  
 130 135 140  
 Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser  
 145 150 155 160  
 Ile Asn Gly Tyr Pro Arg Pro Asn Val Tyr Trp Ile Asn Lys Thr Asp  
 165 170 175  
 Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn  
 180 185 190  
 Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr  
 195 200 205  
 Pro Ser Val Asn Ile Gly Cys Ile Glu Asn Val Leu Leu Gln Gln  
 210 215 220  
 Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp  
 225 230 235 240  
 Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr  
 245 250 255  
 Trp Ser Ile Leu Ala Val Leu Cys Leu Val Val Val Val Ala Val Ala  
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 275 280 285  
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 <213> Homo sapiens

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 ctgcacatgac aaattgcaaa ctctcaaaac caaagcctga gtgagctagt agtattttgg 300  
 gaggaccagc gaaacttggg tctgaatggg gtatacttgg acagtggag cctgagactt 360  
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 acaggaatga tctgcattcca ccagatgaat tctgaactgt tgatcactaa ttgacctgc 540  
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 tcaactatcg agtatgatgg tattatgcag aaatctcaag ataagtctac agaactgtac 720  
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 aactcttata aatgtggaa ccaacaaatg gagagggaag agagtgaaca gaccaaga 1020  
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 aagacatctt catcgacaaa aagtgtatca tgttttaatt taaagagtaa agcccata 1140  
 agtatctatt ttcttacc cctgtctgt aagttctctg gcaacctttt tgtattcttc 1200  
 cagaagacaa aaagacata agctgtcttc agtatggcaa ccaggactcc cttaagtgg 1260  
 aatagcctcc ctgaactcc agctgtcttc gagggagact taattctctt 1320  
 actgtctctt ttaacttcag agcacacta tgggccaagc ccagcttaat ggcctcatg 1380  
 ctggaataaa aatttaggac caataaaaa aaaaaaaaaa aaaa 1424

<210> 121  
 <211> 323  
 <212> PRT  
 <213> Homo sapiens

<400> 121  
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Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val	Leu	Asn	Glu	Val	Tyr	Leu
Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser	Lys	Tyr	Met	Gly	Arg	Thr
Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg	Leu	His	Asn	Leu	Gln	Ile
Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	His	His	Lys	Lys	Pro	Thr
Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser	Glu	Leu	Ser	Val	Leu	Ala
Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile	Ser	Asn	Ile	Thr	Glu	Asn
Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile	His	Gly	Tyr	Pro	Glu	Pro
Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	Ile	Glu	Tyr
Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	Leu	Tyr	Asp
Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	Ser	Asn	Met
Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	Leu	Ser	Ser
Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	Asp	His	Ile
Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	Val	Met	Val
Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Arg	Pro	Arg	Asn	
Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	Ser	Glu	Gln
Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	Asp	Glu	Ala
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Thr	Cys	Phe													

<210> 122  
<211> 1816  
<212> DNA  
<213> Homo sapiens

<400> 122

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cttactgtttt	tctttatcac	ccagatgatt	gggtcagcac	tttttgcgtg	gtatcttcatt	180
agaaggttgg	acaagataga	agatgaaagg	aatcttctatg	aagattttgt	attcatgaaa	240
acgatatacaga	gatgcaaac	aggagaaga	tccttatcct	tactgaactg	tgaggagatt	300
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gaaaaacagct	ttgaaatgca	aaaaggtgat	cagaaatcctc	aaattgcggc	acatgtcata	420
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cttgccaagt	tcagttttgt	ttctttgcgt	gcagttgctt	tcctatggata	atgcatttga	1200
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agaacgcgaa	cccccccccc	cccccccgcc	accctctcgg	acagttattc	attctcttcc	1380

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cccactctctc attacgaaat gactgtattt aaaggaaatc tattgtatct acctgcagtc 1740  
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<210> 123  
<211> 261  
<212> PRT  
<213> Homo sapiens

<400> 123  
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Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg  
35 40 45  
Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val  
50 55 60  
Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser  
65 70 75 80  
Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys  
85 90 95  
Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu  
100 105 110  
Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser  
115 120 125  
Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly  
130 135 140  
Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln  
145 150 155  
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160 165 170  
Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser  
175 180 185 190  
Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala  
195 200 205  
Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His  
210 215 220  
Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn  
225 230 235 240  
Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe  
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Gly Leu Leu Lys Leu  
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<210> 124  
<211> 1879  
<212> DNA  
<213> Homo sapiens

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aaccctctc atccacccc 1879

<210> 125  
<211> 400  
<212> PRT  
<213> Homo sapiens

<400> 125  
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35 40 45  
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35 40 45  
Gln Leu Thr Trp Ser Arg Glu Ser Pro Leu Lys Pro Phe Leu Lys Leu  
50 55 60  
Ser Leu Gly Leu Pro Gly Leu Gly Ile His Met Arg Pro Leu Ala Ser  
65 70 75  
Trp Leu Phe Ile Phe Asn Val Ser Gln Gln Met Gly Gly Phe Tyr Leu  
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115 120 125  
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Ser Ser Pro Ser Gly Lys Leu Met Ser Pro Lys Leu Tyr Val Trp Ala  
145 150 155  
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160 165 170  
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175 180 185  
Gly Ser Thr Leu Trp Leu Ser Cys Gly Val Pro Pro Asp Ser Val Ser  
190 195 200  
Arg Gly Pro Leu Ser Trp Thr His Val His Pro Lys Gly Pro Lys Ser  
205 210 215  
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220 225 230  
Val Met Glu Thr Gly Leu Leu Leu Pro Ala Thr Ala Gln Asp Ala  
235 240 245  
Gly Lys Tyr Tyr Cys His Arg Gly Asn Leu Thr Met Ser Phe His Leu  
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Ser Leu Pro Thr Pro Thr Ser Gly Leu Gly Arg Ala Gln Arg Trp Ala  
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Ala Gly Leu Gly Gly Thr Ala Pro Ser Tyr Gly Asn Pro Ser Ser Asp  
370 375 380  
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465 470 475 480  
Pro His Gly Ser Ala Trp Asp Pro Ser Arg Glu Ala Thr Ser Leu Gly  
485 490 495  
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Leu Arg Ser Ile Arg Gly Gln Gly Pro Asn His Glu Glu Asp Ala  
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<212> DNA

<213> Homo sapiens

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<212> PRT

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Val Lys Gly Lys Met Ile Met Asn Ser Leu Ser Leu Phe Ala Ala Ile  
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 Tyr Pro Pro Lys Lys Val Thr Thr Val Ile Gln Asn Pro Met Pro Ile  
 415 420 425  
 Arg Glu Gly Asp Thr Val Thr Leu Ser Cys Asn Tyr Asn Ser Ser Asn  
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 Glu Met Asn Ile Pro Arg Thr Gly Asp Ala Glu Ser Ser Glu Met Gln  
 740 745 750  
 Arg Pro Pro Arg Thr Cys Asp Thr Val Thr Tyr Ser Ala Leu His  
 755 760 765  
 Lys Arg Gln Val Gly Asp Tyr Glu Asn Val Ile Pro Asp Phe Pro Glu  
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<213> Homo sapiens

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35 40 45
Cys Leu Val Phe Thr Val Ala Thr Ile Met Val Leu Val Val Gln Arg
50 55 60
Thr Asp Ser Ile Pro Asn Ser Pro Asp Asn Val Pro Leu Lys Gly Gly
65 70 75 80
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Lys Ser Trp Ala Tyr Leu Gln Val Ala Lys His Leu Asn Lys Thr Lys
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Leu Ser Trp Asn Lys Asp Gly Ile Leu His Gly Val Arg Tyr Gln Asp
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 165 170 175  
 Cys Glu Ser Gly Met Gln Thr Lys His Val Tyr Gln Asn Leu Ser Gln  
 180 185 190  
 Phe Leu Leu Asp Tyr Leu Gln Val Asn Thr Thr Ile Ser Val Asn Val  
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 35 40 45  
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 Gly Ile Phe Thr Met Gly Ile Ala Leu Leu Gly Cys Val Gly Ala Leu  
 65 70 75  
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 85 90 95  
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 100 105 110  
 Ala Gln Leu Glu Arg Ser Leu Arg Asp Val Val Glu Lys Thr Ile Gln  
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 595 600 605  
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 630 635 640  
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 660 665 670 675  
 Glu Asn Asn Lys Asp Tyr Phe Ser Pro Glu Leu Leu Val Leu Tyr Phe  
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 50 55 60  
 Pro Lys Lys Glu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu  
 65 70 75 80  
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 85 90 95  
 Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr  
 100 105 110  
 Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly  
 115 120 125  
 Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala  
 130 135 140  
 Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu  
 145 150 155 160  
 Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Val Leu Val Arg  
 165 170 175  
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 180 185 190  
 Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln  
 195 200 205  
 Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Gln Leu Val Ser Pro  
 210 215 220  
 Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp  
 225 230 235 240  
 Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp  
 245 250 255  
 Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala  
 260 265 270  
 Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu  
 275 280 285  
 Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr  
 290 295 300  
 Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro  
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 Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro  
 325 330 335  
 Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro  
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 Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser  
 355 360 365  
 Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys  
 370 375 380  
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 435 440 445  
 Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly  
 450 455 460  
 Glu Val Thr Arg Glu Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu  
 465 470 475 480  
 Ile Val Ile Ile Thr Val Val Ala Ala Val Ile Met Gly Thr Ala  
 485 490 495  
 Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr  
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 35 40 45  
 Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser Val Glu Leu  
 50 55 60  
 Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg Arg Arg Ala  
 65 70 75 80  
 Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser Gly Thr Tyr  
 85 90 95  
 Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu Ser Gly Thr  
 100 105 110  
 Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr Glu Ser Thr  
 115 120 125  
 Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser Leu Val Val  
 130 135 140  
 Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg Leu Gln  
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 Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln Ala Phe Leu  
 165 170 175  
 Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu Pro Lys  
 180 185 190  
 Thr Glu Thr  
 195